

```

1  GTCTTCCACCATGCATCGTGGGCTTCTTCTGTGGGTGTTCTCTGCTCGCGGCTG 60
   +-----+-----+-----+-----+-----+-----+
   CAGGAAGGTGATCGTACGACGACCCGAGAGAGACACCGCACAGACACGCGCGAC
   M H S L G F F S V A C S L L A A A -
   +-----+-----+-----+-----+-----+-----+
61  CGCTGCTCCGGGTCTCTGGGAGGCGCCGCGCGCGCTTCGAGTCCGACTCG
   +-----+-----+-----+-----+-----+-----+
   GCGACGAGGCCAGAGCGCTCCGCGGGCGGCGCGCGGAGCTCAGGCTGAGC
   L L P G P R E A P A A A A A F E S G L D -
   +-----+-----+-----+-----+-----+-----+
121 ACCTCTCGGACGCGGAGCCCGGAGCGGCGGAGCCACGGCTTATGCAAGCAAAGATCTGG
   +-----+-----+-----+-----+-----+-----+
   TGGAGAGCCTGCGCCTCGGCTGCGCGCGCTCCGGTGCCGAATACGTTGTTCTAGACC
   L S D A E P D A G E A T A Y A S K D L E -
   +-----+-----+-----+-----+-----+-----+
181 AGGAGCAGTTACGGTCTGTGTCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAT
   +-----+-----+-----+-----+-----+-----+
   TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTACATGAGATGGGTCTTA
   E Q L R S V S V D E L M T V L Y P E Y -
   +-----+-----+-----+-----+-----+-----+
241 ATTGAAATGTACAAGTGCAGCTAAGGAAAGGAGGCTGGCAACATACAGAGAACAGG
   +-----+-----+-----+-----+-----+-----+
   TAACCTTTACATGTTACAGTCGATTCCTTCCGCCCGCTGTATGTCTCTTGTC
   W K M Y K C Q L R K G G W Q H N R E Q A -
   +-----+-----+-----+-----+-----+-----+
300 CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTAATAACAG

```

Fig. 1A

MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

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301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
    GGTGGAGTTGAGTTCCTGTCCTCTTGATATTTTAAACGACGTCGGTAAATATTATGTC
      N L N S R T E E T I K F A A A H Y N T E -
    AGATCTTGAAGAATATGATGAATGAGTGGAGAAAAGACTCAATGCATGCCACGGGAGGTGT
361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
    TCTAGAACCTTTTCATPACTATTACTCACCTCTTTCTGAGTTAGTACGTTGCCCTCCACA
      I L K S I D N E W R K T Q C M P R E V C -
    GTATAGATGTGGGAAGGAGTTTGGAGTCGGACAAACACCTCTTTTAAACCTCCATGTG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
    CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
      I D V G K E F G V A T N T F F K P C V -
    TGTCCGTCTACAGATGTGGGGTTGCTGCAATAGTGAAGGGCTGCAGTGCATGAACACCA
481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
    ACAGGCGAGATGCTACACCCCAAGCAGCGTTATCACTCCCGACGTCACGTACTTGTGGT
      S V Y R C G C C N S E G L Q C M N T S -
    GCACGACTACCTCAGCACACGTTATTTGAATATACAGTGCCTCTCTCAAGGCCCA
541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
    CGTGCTCGATGGAGTCGTTCTGCAATAAATTTAATGTCACGGAGAGAGAGTCCCGGGT
      T S Y L S K T L F E I T V P L S Q G P K -
    AACAGTAAACAATCAGTTTTTGCCAAATCACACTTCCTGCCGATGCATGCTAAACTGGATG
601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
    TTGGTCATTTGAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
      P V T I S F A N H T S C R C M S K L D V -

```

MATCH WITH FIG. 1C

Fig. 1B

MATCH WITH FIG. 1B

```

661 TTTACAGACAGTTTCATTCCTATTTAGACGTTCCCTGCCAGCAACACTACACACGTGTC 720
    +-----+-----+-----+-----+-----+-----+
    AATGTCTGTTCACAGTAAGTAATAATCTGCAAGGACGGTCGTGTGCATGGTGTACACAG
    Y R Q V H S I I R S L P A T L P Q C Q -
    AGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATTAATCACATCTGCAGATGCC 780
    +-----+-----+-----+-----+-----+-----+
    TCCGTCGCTTGTCTGGACGGGTGGTTAATGTACACCTTATTAGTTAGACGCTTACGG
    A A N K T C P T N Y M W N N H I C R C L -
    TGGCTCAGGAAGATTTTATGTCTTCTCGATGCTGGAGATGACTCAACAGATGGATTCC 840
    +-----+-----+-----+-----+-----+-----+
    ACCGAGTCTCTTAAATAACAAAAGGAGCCTAGACCTCTACTGAGTTGCTTACCTAAG
    A Q E D F M F S S D A G D D S T D G F H -
    ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCTAGTGTGTCTGCAGAG 900
    +-----+-----+-----+-----+-----+-----+
    TACTGTAGACACCTGGTTGTCTCGACCTTCTCTGGACAGTCAACACAGACGCTCTC
    D I C G P N K E L D E E T C C V C R A -
    CGGGGCTTCGGCCTCCAGCTGTGGACCCCAAGACTAGACAGAACTCATGCCAGT 960
    +-----+-----+-----+-----+-----+-----+
    GCCCCAGCCGGACGGTCGACACCTGGGTGTTCTTGATCTGTCTTTGAGTACGGTCA
    G L R P A S C G P H K E L D R N S C Q C -
    GTGTCTGTAAAAACAACACTCTCCCAAGCAATGTGGGGCCAAACCGAAGATTGTGAGAA 1020
    +-----+-----+-----+-----+-----+-----+
    CACAGACATTTTGTGTGAGAAGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT

```

Fig. 1C

MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

V C K N K L F P S Q C G A N R E F D E N -
ACACATGCCAGTGTGTATGTAAGAAGAACCTGCCCCAGAAATCAACCCCTAAATCTGGAA 1080

1021

T C C Q C C V C K R T C P R N Q P L N P G K -
TGTGTACGGTCACACATACATTTCTTGGACGGGGCTTTAGTTGGGATTTAGGACCTT

AAATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTGTATAAAGGAAAGAGTTC

7081

TTACACGGACCTTACATGCTTTTCAGGTCTTTACGAACAATTTCTTCTTCAAGG
C A C E C T E S P Q K C L L K G K K F H -

ACCACCAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAGGCTTGTGAGC
1200

1741

H Q T C S C Y R R P C T N R Q K A C E P -
TGGTGGTTGTACGTCGACAATGCTGCCGGTACATGCTGGGGTCTTCGGAACACTCG

CAGGATTTTCATATAGTGAAGAGTGTGTCGTTGTGTCCCTTCATATATGGCAAGACCAC

1201

GTCTCTAAAAGTATATCATTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
G F S Y S F E V C R C V P S Y W Q R P Q -

.....TCCGAAACTGTGT

Fig. 1D

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

[illegible]

Fig. 1E

	1	50
Pdgfa	.MRTLACLLL LGCYLAVHL AEEAIPREV IERLARSQIH SIRDLORLLE	
Pdgfb	MNRWA.LFL SLCCYLRVS AEGDPIPEEL YEMLSOHSIR SFDDLORLLH	
VegfMNFLL SWHMSLALL LY..... LHHAKWSQA	
Vegf2MTV LYPEYMKMYK CQ..... LRGGWQHVN	
	51	100
Pdgfa	IDSVCSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSL.....EEAVP	
Pdgfb	GDP GEEDGA ELDLNMTRSH SGGELES... LARGRRSLG SLTIAEPAMI	
Vegf	APMAE.....CGGQ NHHEVVKFMD VYQR.....	
Vegf2	REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....	
	101	150
Pdgfa	AVCKTRTVIY EIPRSQVDPT SANFLIWPCC VEVKRCTGCC NTSSVKQPS	
Pdgfb	AECKTRTEVF EISRRLLDRT NANFLVWPPC VEVRQSCGCC MNRNVQCRPT	
Vegf	SYCHPIETLV DIFOEYPOEI ..EYIFKPC VPLMRGCGCC NDEGLECMPT	
Vegf2	TQMPREVC I DVGKEFGVAT ..NTFFKPPC VSVYRCGCGCC NSEGLQAMNT	
	151	200
Pdgfa	RVHHRVKVA KVEYRKKPK LKEVQVRLEE HLECA..... AT.....	
Pdgfb	QVQLRPVQVR KIEIVRKKPI FKKTATVLED HLAACK... ETVAARPVT	
Vegf	EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKQEPKPK DRARDEKKS	
Vegf2	STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSDQMSKL DYYRQVHSLI	

Fig. 2A

```

201      TSLNPD YREEDTVR.
Pdffa ..... RTVVRPPK GKHRKFHITH DKTALKETLG
Pdffb RSPGSGEQR AKTPQTRVTI
Vegf RGK ..... .GKGQKRKRK KSRYSWSVY VGARCCCLMPW SLPQPH
Vegf2 RRSLLPATLPQ COAANKTPT NYMNNHICR CLAQEDFMFS SDAGDDSDTG
250

251
Pdffa .....
Pdffb A..... CSE RRKHLFVDDP QTCKSCSKNT
Vegf .....CGP..... RAGLRPASCG PHKEL...DR NSCOCVCKNK
Vegf2 FHDTCGPKE LDEETCCVC RAGLRPASCG PHKEL...DR NSCOCVCKNK
300

301
Pdffa .....
Pdffb .....DSRCKARQ LELNERTCRC DKPRR.....
Vegf .....LFPSCGANR .EFDENTCOC VCKRTCPRNQ PLNPKKACE CTESPKCLL
Vegf2 .....
350

351
Pdffa .....
Pdffb .....
Vegf .....
Vegf2 KGKKFHQTC SCYRRPCTNR OKACEPGFSY SEEVCRCPVS YWOPQMS
398

```

Fig. 2B

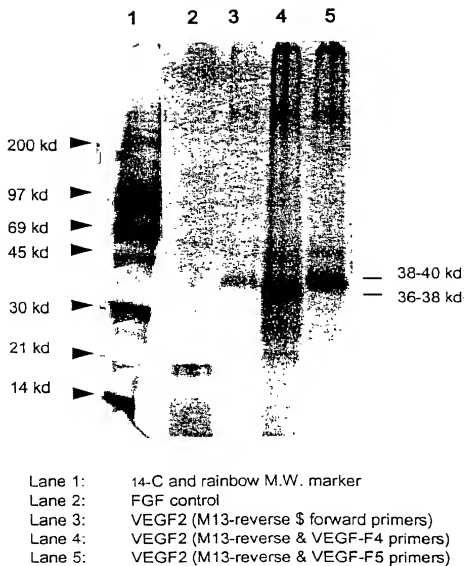


Fig. 3

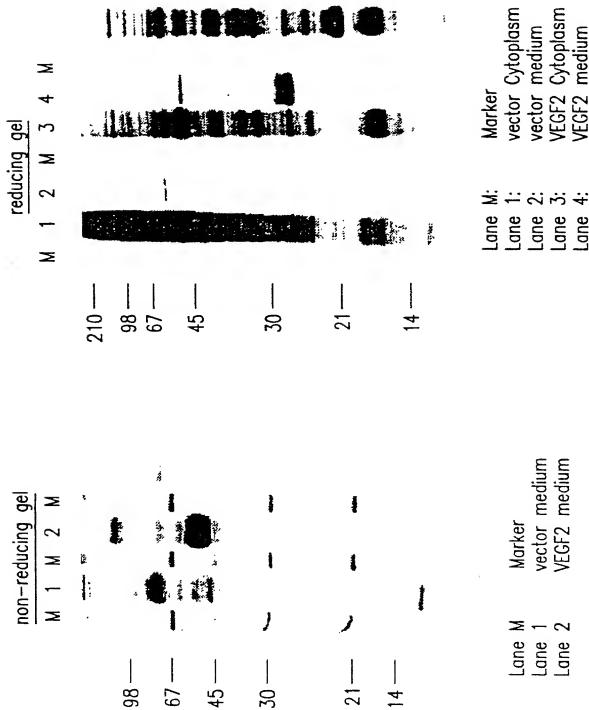
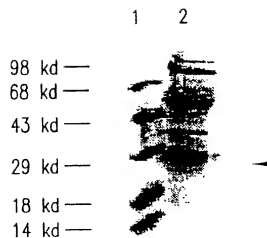


Fig. 4

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Lane 1: Molecular weight marker
Lane 2: Precipitates containing VEGF2.

Fig. 5

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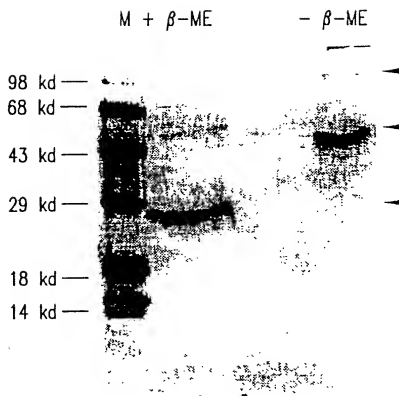


Fig. 6

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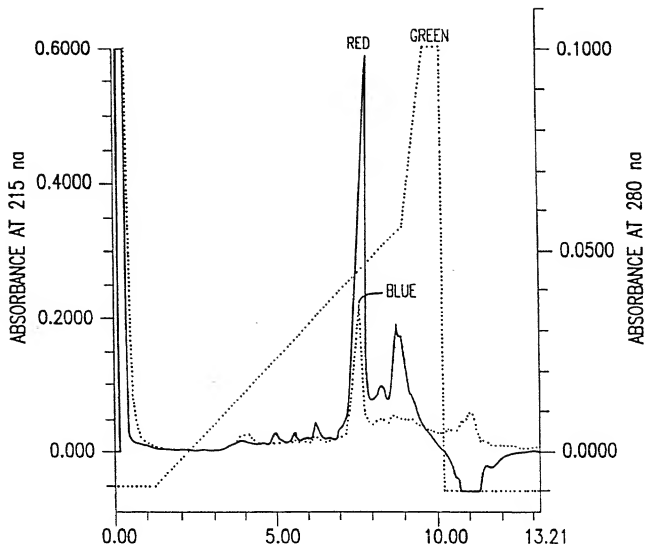


Fig. 7

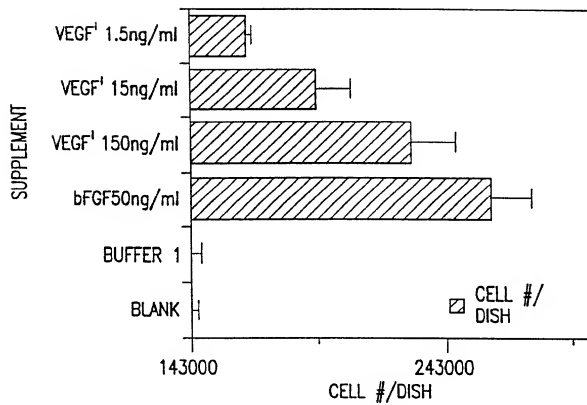


Fig. 8

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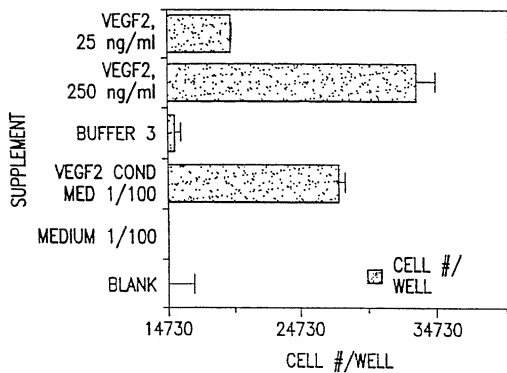


Fig. 9